

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 14, 2003, 00:02:20 ; Search time 3456 Seconds  
(without alignments)  
10047.200 Million cell updates/sec

Title: US-09-698-781-2  
Perfect score: 2144  
Sequence: 1 tgaatgaacaatactcatc.....gaaaaaaaaaaaaaaaaa 2144

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estm:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vit:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rnd:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	583.8	27.2	587	14	BM993763 UI-H-DF1-
2	541.8	25.3	547	9	AL703262 DKFP686K
C 3	516.4	24.1	518	12	BF446166 7p3c05.x
C 4	487.4	22.7	516	9	AA523498 n167h04.s
C 5	485.8	22.7	489	10	AA468294 h635f04.x
C 6	483.4	22.5	485	10	BE673586 7d39g01.x

Result No.	Score	Query Match	Length	ID	Description
C 7	469.8	21.9	485	12	BE855975
8	463	21.6	1108	13	BM552843
9	459	21.3	1037	13	BM554122
C 10	455.6	21.3	483	9	AT791464
C 11	453.6	21.2	462	12	BE897377
12	450.2	21.0	455	9	AT791346
13	449.2	21.0	457	9	AA885547
14	448.4	20.9	450	12	BE897404
15	444.6	20.7	1063	13	BM559790
C 16	442.2	20.6	464	12	BE897412
17	442	20.6	464	12	BE897410
C 18	438.4	20.4	461	9	AT732509
C 19	436.2	20.3	443	12	BE897401
20	429.6	20.0	445	9	AA888237
21	422.8	19.7	428	9	AA886557
22	422.4	19.7	803	13	BI826346
23	421.8	19.7	781	13	BI829771
24	421.4	19.7	808	13	BI826697
C 25	420.6	19.6	427	9	AT400952
26	418.6	19.5	454	12	BE897368
27	418.4	19.5	420	12	BE897378
C 28	406.4	19.0	419	10	AW236196
C 29	398.6	18.6	784	13	BI825564
C 30	398	18.6	406	12	BE897379
C 31	397.4	18.5	413	9	AT732549
C 32	397.4	18.5	419	9	AT791304
33	397.4	18.5	439	9	AT791506
C 34	389.8	18.2	393	9	AA522856
35	387.8	18.1	864	13	BI605044
36	386.6	18.0	728	13	BI827352
C 37	386.2	18.0	392	9	AA522850
38	378.4	17.6	804	13	BI830749
39	378	17.6	906	13	BI826010
40	374.6	17.5	760	12	BG722432
41	373.8	17.4	401	12	BE897366
42	371	17.3	801	13	BI831850
43	370.8	17.3	417	9	AA876668
44	369.4	17.2	742	12	BG723701
C 45	368.8	17.2	372	9	AA877068

## ALIGNMENTS

RESULT 1  
LOCUS BM993763/C  
DEFINITION UI-H-DF1-eug-b-15-0-UI-s1 NCI-CGAP-DF1 Homo sapiens CDNA clone  
IMAGE:5868974.3', mRNA sequence.  
ACCESSION BM993763  
VERSION BM993763.1 GI:19715416  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 587)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).  
JOURNAL Tumor Gene Index  
COMMENT Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Dr. Jose Mercende  
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be found  
through the I.M.A.G.E. Consortium/LINL at: http://lmage.llnl.gov  
The following repetitive elements were found in this CDNA  
sequence: 28-581>LIMC3#LINE/L1 (matched complement)  
Seq primer: M13 FORWARD  
POLYA=yes.

## FEATURES

Location/Qualifiers

1. 587  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5868974"  
 /clone.lib="NCI-CGAP.DP1"  
 /tissue.type="Subchondral Bone"  
 /dev.stage="Adult"  
 /lab.host="DH10B (Life Technologies)"  
 /note="Organ: Bone; Vector: p773-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; NCI-CGAP.DP1 is a normalized cDNA library containing the following tissue(s): Subchondral Bone. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTTAAAGCTC.  
 TAG.lib=UI-H-DP1  
 TAG.tissue=Subchondral bone  
 TAG\_SEQ=GTAAAGCTC"  
 BASE COUNT 150 a 113 c 87 g 237 t  
 ORIGIN

## Query Match

Best Local Similarity 99.7%; Pred. No. 3.3e-81;  
 Matches 585; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1557 GAGTGGAGTATGAAAGGAAACATAGTACTTACAGGGGAGAAATGACAAATGACG 1616  
 DB 587 GAGTGGAGTATGAAAGGAAACATAGTACTTACAGGGGAGAAATGACAAATGACG 528  
 OY 1617 TCTTACCAGATGACAAATTAACGTCACAGTGATAGTATTCAGATTTGTTCTACA 1676  
 DB 527 TCTTACCAGATGACAAATTAACGTCACAGTGATAGTATTCAGATTTGTTCTACA 468  
 OY 1677 TAATCTTTCTAAATAATTCATATCCCAATCATATGATGATGATGATGATGATGAT 1736  
 DB 467 TAATCTTTCTAAATAATTCATATCCCAATCATATGATGATGATGATGATGATGAT 408  
 OY 1737 AAGTTGAAGGACATCTCAAAATATCCCTGGGGTATTTAGATATTCCTCAAACTGT 1796  
 DB 407 AAGTTGAAGGACATCTCAAAATATCCCTGGGGTATTTAGATATTCCTCAAACTGT 348  
 OY 1797 AAAAAATCATGAAATTAAGGGATCCTGAGAAACATCACAGACCATGAGACTAAGGA 1856  
 DB 347 AAAAAATCATGAAATTAAGGGATCCTGAGAAACATCACAGACCATGAGACTAAGGA 288  
 OY 1857 GACATGTGAGCAATGCAATGCTGCTTGTGATCAGATCCCGAACAAGAAAGTCCAG 1916  
 DB 287 GACATGTGAGCAATGCAATGCTGCTTGTGATCAGATCCCGAACAAGAAAGTCCAG 228  
 OY 1917 TAATGAAAAAACTGATGAAGTCTGAATAGAAATCTGAGATATTTTAAACAGTAGTGTGAT 1976  
 DB 227 TAATGAAAAAACTGATGAAGTCTGAATAGAAATCTGAGATATTTTAAACAGTAGTGTGAT 168  
 OY 1977 TTCTTAATCTTGACAAATATAGCAGGATATATAGATGATATACGTTAGAGAACTGA 2036  
 DB 167 TTCTTAATCTTGACAAATATAGCAGGATATATAGATGATATACGTTAGAGAACTGA 108  
 OY 2037 CTGGGTGAGGGCTATCTAGGAATCTCTGTACTATCTTACCAATTTTGGGTAAGCTTA 2096  
 DB 107 CTGGGTGAGGGCTATCTAGGAATCTCTGTACTATCTTACCAATTTTGGGTAAGCTTA 48  
 OY 2097 GAAACCAATGCAAAATTAAGATATCTGAAAAAATTTTAAAAA 2143  
 DB 47 GAAACCAATGCAAAATTAAGATATCTGAAAAAATTTTAAAAA 1

## RESULT 2

AL703262

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AL703262 547 bp mRNA linear EST 22-MAR-2002  
 DKFZp666K1819.f1 686 (synonym: hlc3) Homo sapiens cDNA clone  
 DKFZp666K1819.5', mRNA sequence.  
 AL703262  
 AL703262.1 GI:19686617  
 EST.  
 human.  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 547)  
 Poustka,A., Wellenreuther,R., Mewes,H.W., Well,B. and Wiemann,S.).  
 EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Well,B. and Wiemann,  
 S.)  
 Unpublished (1999)  
 Contact: Poustka A.J.  
 Department Leinrach  
 Max-Planck-Institute for Molecular Genetics  
 Ihnestrasse 73, 14195 Berlin, Germany  
 Tel: +49-30-84131623  
 Fax: +49-30-84131128  
 Email: poustka@mpg-berlin-dahlem.mpg.de  
 This is the 5' sequence of the clone insert  
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
 Heidelberg/Germany) within the cDNA sequencing consortium of the  
 German Genome Project.  
 No sl sequence available.  
 This clone (DKFZp666K1819) is available at the RZPD in Berlin.  
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.  
 Location/Qualifiers  
 1. 547  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="DKFZp666K1819"  
 /clone.lib="686 (synonym: hlc3)"  
 /tissue.type="human skeletal muscle"  
 /dev.stage="adult"  
 /lab.host="DH10B"  
 /note="Vector: pTriplex2; Site\_1: SfiI; Site\_2: SfiIb;  
 cDNA-collection"  
 BASE COUNT 170 a 120 c 120 g 137 t  
 ORIGIN

Query Match 25.3%; Score 541.8; DB 9; Length 547;  
 Best Local Similarity 99.6%; Pred. No. 1.1e-74;  
 Matches 543; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GATGAAACAAATCTTCACTGCTGCTGGAACACCTGAAATGACATTTTCCAGTGT 61  
 DB 3 GATGAAACAAATCTTCACTGCTGCTGGAACACCTGAAATGACATTTTCCAGTGT 62  
 OY 62 GTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 121  
 DB 63 GTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 122  
 OY 122 TTTTACTGTTTGTAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 181  
 DB 123 TTTTACTGTTTGTAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 182  
 OY 182 TGAATGAGAGAGATATCTCCCTGCGCAACATGCTGAAAGATGGAATGGAACA 241  
 DB 183 TGAATGAGAGAGATATCTCCCTGCGCAACATGCTGAAAGATGGAATGGAACA 242  
 OY 242 AGAGGCTGACGCAATGCGCAAAAGTGGGCAAAACAGTGCATTTACAGACAGTAACCC 301  
 DB 243 AGAGGCTGACGCAATGCGCAAAAGTGGGCAAAACAGTGCATTTACAGACAGTAACCC 302

QY 302 AAGGATCGAATGACAACTCTAAATGTGTGAGATCTTACATGTCAAGTCCCCAG 361  
DB 303 AAGGATCGAATGACAACTCTAAATGTGTGAGATCTTACATGTCAAGTCCCCAG 362  
QY 362 CTCATGTGCACAGCAATCCAAAGCTGTTGAGAGTACATGATTTTGACTTGGTGT 421  
DB 363 CTCATGTGCACAGCAATCCAAAGCTGTTGAGAGTACATGATTTTGACTTGGTGT 422  
QY 422 AGGGCCAAAGACTCCCAAGCGAGTGTGACATATACAGAGTGTGGTGTCTTC 481  
DB 423 AGGGCCAAAGACTCCCAAGCGAGTGTGACATATACAGAGTGTGGTGTCTTC 482  
QY 482 ATACTCTGTGGATGTGGAATGCTTACTGTCCCAATCAAAAGTTCTAAATACTACTA 541  
DB 483 ATACTCTGTGGATGTGGAATGCTTACTGTCCCAATCAAAAGTTCTAAATACTACTA 542  
QY 542 TGTGT 546  
DB 543 TGTGT 547

RESULT 3  
LOCUS BF46166 518 bp mRNA linear EST 01-DEC-2000  
DEFINITION 7p3c05.x1 NCI\_CGAP\_P128 Homo sapiens cDNA clone IMAGE:3647601 3',  
mRNA sequence.  
ACCESSION BF46166  
VERSION BF46166.1 GI:11511304  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 518)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaaps-rt@mail.nih.gov  
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/BLN, send email to:  
info@image.lnl.gov  
Info@image.lnl.gov  
Seq primer: -400p from Glibco  
High quality sequence stop: 465.

## FEATURES

source  
1. 518  
Location/Qualifiers

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="3647601"  
/clone\_lib="NCI\_CGAP\_P128"  
/sex="male"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)  
with a modified polylinker; Plasmid DNA from the  
normalized library NCI\_CGAP\_P128 was prepared, and s  
circles were made in vitro. Following HAP purification,  
this DNA was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from a pool  
of 5,000 clones made from the same library (clonoids  
983608-986759, 1101192-1101959, and 1217928-1220615).  
Subtraction by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 141 a 96 c 82 g 199 t  
ORIGIN

Query Match 24.1%; Score 516.4; DB 12; Length 518;  
Best Local Similarity 99.8%; Pred. No. 9.6e-71;

Matches 517: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1613 GACGCTTCACCAAGTGCATCAAAATTAACGTACAGATGATGATTCATGATTTGTTTC 1672  
DB 518 GACGCTTCACCAAGTGCATCAAAATTAACGTACAGATGATGATTCATGATTTGTTTC 459  
QY 1673 TAGATAATCTTTCTAAATTAATTCATATCCCAATCTAATATGAGTAAACATCCAGCA 1732  
DB 458 TAGATAATCTTTCTAAATTAATTCATATCCCAATCTAATATGAGTAAACATCCAGCA 399  
QY 1733 ACTCAAGTTGAAGGACATTTCTCAAAATATCCCTGGGGATTTTATGAGATTTCTCAAAA 1792  
DB 398 ACTCAAGTTGAAGGACATTTCTCAAAATATCCCTGGGGATTTTATGAGATTTCTCAAAA 339  
QY 1793 CTGTAAATATCATGGAATAATAGGAAATCCGTGAGAAACATGACAGACATGAGACTA 1852  
DB 338 CTGTAAATATCATGGAATAATAGGAAATCCGTGAGAAACATGACAGACATGAGACTA 279  
QY 1853 AGGAGACATGTGAGCCAAATGCAATGTGCTTCTTGATCAGATCCTGGAACAGAAAAAGA 1912  
DB 278 AGGAGACATGTGAGCCAAATGCAATGTGCTTCTTGATCAGATCCTGGAACAGAAAAAGA 219  
QY 1913 TCAGTAATGAAAAAACTGATGAGTCTGAATGATCTGAGATATTTTACAGTAGTGT 1972  
DB 218 TCAGTAATGAAAAAACTGATGAGTCTGAATGATCTGAGATATTTTACAGTAGTGT 159  
QY 1973 TCATTTCTTATCTTGACAAATATAGCAGGTAATGATGATGATGATGATGATGATGAT 2032  
DB 158 TCATTTCTTATCTTGACAAATATAGCAGGTAATGATGATGATGATGATGATGATGAT 99  
QY 2033 GAACTGGGTGAGGCTATCTAGAAATCTCTGATCTATCTTACCAATTTTGGTAACT 2092  
DB 98 GAACTGGGTGAGGCTATCTAGAAATCTCTGATCTATCTTACCAATTTTGGTAACT 39  
QY 2093 CTAAAGAACCATGCAAAATTAAGTACTTGAAAAA 2110  
DB 38 CTAAAGAACCATGCAAAATTAAGTACTTGAAAAA 1

## RESULT 4

LOCUS AA523498 516 bp mRNA linear EST 05-AUG-1997  
DEFINITION n167h04.s1 NCI\_CGAP\_P12 Homo sapiens cDNA clone IMAGE:981943, mRNA  
sequence.  
ACCESSION AA523498  
VERSION AA523498.1 GI:2264210  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 516)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaaps-rt@mail.nih.gov  
Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,  
Rodrigo F. Chuang, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: David B. Kitzman, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/BLN at:  
www.bio.lnl.gov/dbip/image/image.html  
Insert Length: 505 Std Error: 0.00  
Seq primer: -40m3 fwd. ET from Amersham  
High quality sequence stop: 395.

## FEATURES

source  
1. 516  
Location/Qualifiers

/organism="Homo sapiens"  
/db\_xref="taxon:9606"

```

/clone="IMAGE:981943"
/clone.lib="NCI_CGAP_Pr12"
/sex="male"
/tissue_type="metastatic prostate bone lesion"
/lab_host="DH10B"
/Note="Vector: PAMP10; mRNA made from metastatic prostate
lesion of the bone, cDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel,
average insert size 600 bp. Library made by D. Krizman,
NIH."
BASE COUNT      135 a      98 c      81 g      202 t
ORIGIN

```

```

Query Match      22.7% Score 487.4; DB 9; Length 516;
Best Local Similarity 98.6%; Pred. No. 3e-66;
Matches 502; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

```

```

OY 1635 AATTACGTCACCA-GTGTATAGTCATTCAGATTGTTCTAGATATCTTTCTAAAAAT 1693
DB 516 AATTACGTCACCGAGGATAGTCATTCAGATTGTTCTAGATATCTTTCTAAAAAT 457
OY 1694 CATATCCCATCTATATATGAGCTAAACATCCAGCAAACTCAAGTTGAAAGACATTC 1753
DB 456 CATATCCCATCTATATATGAGCTAAACATCCAGCAAACTCAAGTTGAAAGACATTC 397
OY 1754 ACAAAATATCCCTGGGGTATTTTATAGTATCTTCCCTCAAACTGTAATAATCATGAAATA 1813
DB 396 ACAAAATATCCCTGGGGTATTTTATAGTATCTTCCCTCAAACTGTAATAATCATGAAATA 337
OY 1814 AGGAATCTGAGAAACATCAGACACCATGAGACTAGAGACATGTGAGCCAAATG 1873
DB 336 AGGAATCTGAGAAACATCAGACACCATGAGACTAGAGACATGTGAGCCAAATG 277
OY 1874 CAATGTGTTCTTGATAGATCTCTGGAACAGAAAAAGATCAGTAATGAAAAACTGATG 1933
DB 276 CAATGTGTTCTTGATAGATCTCTGGAACAGAAAAAGATCAGTAATGAAAAACTGATG 217
OY 1934 AAGTCGATAGATCTGAGTATTTTATACAGTGTGATCTTCTTAATCTTACAAA 1993
DB 216 AAGTCGATAGATCTGAGTATTTTATACAGTGTGATCTTCTTAATCTTACAAA 157
OY 1994 TATAGCAGGATATGATAGATGATACGTTAGAGAACTGAACTGGGTGAGGCTATCT 2053
DB 156 TATAGCAGGATATGATAGATGATACGTTAGAGAACTGAACTGGGTGAGGCTATCT 97
OY 2054 AGGAATCTCTGATCTATCTTACCAATTTTGGTAACTGTAAGAAACCAATGCAAAATA 2113
DB 96 AGGAATCTCTGATCTATCTTACCAAAATTTTGGTAACTGTAAGAAACCAATGCAAAATC 37
OY 2114 AAAAGTATCTGAAAAAATTTTAAAAA 2142
DB 36 CGAAGTCTCTGAAAAAATTTTAAAAA 8

```

```

RESULT 5
AM468294/c 489 bp mRNA linear EST 24-FEB-2000
LOCUS he35f04.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2921023 3'
DEFINITION mRNA sequence.
ACCESSION AM468294
VERSION AM468294.1 GI:7038400
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

```

```

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabp-s.r@mail.nih.gov

```

```

FEATURES
SOURCE
1. 489
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2921023"
/clone.lib="NCI_CGAP_CML1"
/tissue_type="myeloid cells, 18 pooled CML cases, BCR/ABL
rearrangement positive, includes both chronic phase and
myeloid blast crisis"
/lab_host="DH10B"
/Note="Organ: whole blood; Vector: pCMV-Sport6; Site: 1;
Salt: Site 2; Note: Cloned unidirectionally. Primer:
Oligo dT. Library constructed by Life Technologies."
BASE COUNT      136 a      92 c      77 g      184 t
ORIGIN

```

```

Query Match      22.7% Score 485.8; DB 10; Length 489;
Best Local Similarity 99.6%; Pred. No. 5.4e-66;
Matches 487; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

OY 1637 TTACGTCACGATGATAGTCATTCAGATTGTTCTAGATATCTTTCTAAAAATCAT 1696
DB 489 TTACGTCACGATGATAGTCATTCAGATTGTTCTAGATATCTTTCTAAAAATCAT 430
OY 1697 AATCCCATCTAATATATAGCTAAACATCCAGCAAACTCAAGTTGAAAGACATTC 1756
DB 429 AATCCCATCTAATATATAGCTAAACATCCAGCAAACTCAAGTTGAAAGACATTC 370
OY 1757 AAATATCCCTGGGGTATTTTATAGTATCTTCCCTCAAACTGTAATAATCATGAAATA 1816
DB 369 AAATATCCCTGGGGTATTTTATAGTATCTTCCCTCAAACTGTAATAATCATGAAATA 310
OY 1817 GAATCTGAGAAACATCAGACACCATGAGACTAGAGACATGTGAGCCAAATGCA 1876
DB 309 GAATCTGAGAAACATCAGACACCATGAGACTAGAGACATGTGAGCCAAATGCA 250
OY 1877 TGTGCTCTTGATAGATCTCTGGAACAGAAAAAGATCAGTAATGAAAAACTGATGAG 1936
DB 249 TGTGCTCTTGATAGATCTCTGGAACAGAAAAAGATCAGTAATGAAAAACTGATGAG 190
OY 1937 TCTGAATAGATCTGAGTATTTTATACAGTGTGATCTTCTTAATCTTGAACAAATAT 1996
DB 189 TCTGAATAGATCTGAGTATTTTATACAGTGTGATCTTCTTAATCTTGAACAAATAT 130
OY 1997 AGCAGGATATGATAGATGATACGTTAGAGAACTGAACTGGGTGAGGCTATCTAGG 2056
DB 129 AGCAGGATATGATAGATGATACGTTAGAGAACTGAACTGGGTGAGGCTATCTAGG 70
OY 2057 AATCTCTGATCTATCTTACCAATTTTGGTAACTGTAAGAAACCAATGCAAAATA 2116
DB 69 AATCTCTGATCTATCTTACCAAAATTTTGGTAACTGTAAGAAACCAATGCAAAATA 10
OY 2117 AGTATCTTG 2125
DB 9 AGTATCTTG 1

```

```

RESULT 6
BE673586/c 485 bp mRNA linear EST 08-SEP-2000
LOCUS BE673586
DEFINITION 7d39g01.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3249848 3'
ACCESSION BE673586

```



Fri Mar 14 14:00:05 2003

us-09-6988-781-2.rst

Page 6

RESULT 8	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1767	GGGGATATTTAGAGTATTCCTCAAAACSTATAAAATCATGGAATAATGAAGGAATCCTG	1108 bp	BM552843	1			Homo sapiens					
365	GGGGATATTTAGAGTATTCCTCAAAACSTATAAAATCATGGAATAATGAAGGAATCCTG											
1827	AAACATATCAGACACACATGAGACTAAGGAGACATGTGAGCCAAATGCATGTGCTTCT											
305	AAACATATCAGACACACATGAGACTAAGGAGACATGTGAGCCAAATGCATGTGCTTCT											
1887	GGAT-CAAGTCTCGAAGCAAGAAAGATTCAGTATATGAAAAAAGCTGATGAGTCTGATAG											
245	GGATCGGATCGCTGGAACAGAAAAAGATCAGTAAAGAAAAAAGCTGATGAGTCTGATAG											
1946	AATCTGGAGTATTTTAAACAGTACGATGTTGATTTCTTAATCTTGACAATATGACAGGGTA											
185	AATCTGGAGTATTTTAAACAGTACGATGTTGATTTCTTAATCTTGACAATATGACAGGGTA											
2006	ATGTAGATGATATACGTTAGAGAAAAGTGAAGGCTGAGGCTATCTAGAAATCTCTG											
125	AGTATAGATGATATACGTTAGAGAAAAGTGAAGGCTGAGGCTATCTAGAAATCTCTG											
2066	TACTATCTTACCAATTTTCGGTAGTCTAACAAGCAATGCAGAAATATGAATCTTG											
65	TACTATCTTACCAATTTTCGGTAGTCTAACAAGCAATGCAGAAATATGAATCTTG											
2126	AAAAA 2130											
5	AAAAA 1											
BM552843	AGENCOURT_6542520 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742685											
BM552843	5', mRNA sequence.											
BM552843.1	GI:18791053											
EST.												
human.												
Homo sapiens												
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;												
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.												
1 (bases 1 to 1108)												
NIH-MGC http://mgc.nci.nih.gov/.												
National Institutes of Health, Mammalian Gene Collection (MGC)												
Unpublished (1999)												
Contact: Robert Strausberg, Ph.D.												
Email: cgapds-remail.nih.gov												
Tissue Procurement: Life Technologies, Inc.												
cDNA Library Preparation: Life Technologies, Inc.												
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)												
DNA sequencing by: Agencourt Bioscience Corporation												
Clone distribution: MGC clone distribution information can be												
found through the I.M.A.G.E. Consortium/LNLN at:												
http://image.lnl.gov												
plate: LAM12761 row: d column: 14												
High quality sequence status: 700.												
Location/Qualifiers												
1. 1108												
/organism="Homo sapiens"												
/db_xref="taxon:9606"												
/clone="IMAGE:5742685"												
/clone_id="NIH_MGC_119"												
/tissue_type="medulla"												

BASE COUNT	341 a	236 c	235 g	291 t	5 others
ORIGIN					
Query Match	21.6%	Score 463;	DB 13;	Length 1108;	
Best Local Similarity	76.0%;	Pred. No. 1.3e-62;	Mismatches 595;	Conservative 0;	Mismatches 184; Indels 4; Gaps 2.
Dy	51	TTCOCAGTCTGTGTTGCCGTGGTGCGTCCATCTTCCACCAATAAGAGAT	110		
Db	145	TTACTACCGGTGTTGTTTGGTACTGTGCTGCTTCACTTACTCACA--GAAGA	201		
OY	111	AAGATCCGCCTTTTACTGCTTTGTTAACACCACCAACAAAGTGCMAAGGAGATTGG	170		
Db	202	AAGGATCCCCGCTTTTACTCTTTGTTAACACCACCAAGTGCMAAGGAGATTGG	261		
OY	171	AATTAAGCAAATGAAGTGAAGAGACAGTATCTCCCCTCCAGAAACATGCTGAAGATG	230		
Db	262	AATTAACCAATGAAGTGAAGAGAGTATCTCCCCTCCAGAAACATGCTGAAGATG	321		
OY	231	GATGAGAACAAAGAGGCTGCACCAAAATGCGCCAAAAGTGGGCAACAGCATTTACAGA	290		
Db	322	GATGAGAGCAGAGAGTAGTAAACAGATGCGCCAAAAGTGGGCAACAGCATTTACAGA	381		
OY	291	CACAGTAAACCAAGAGTGAATGACAGCTTAAATGTGGTGAATCTTACATGTCA	350		
Db	382	CATAGTGAATCCAGAGAGCAGCAAAACAGATTAAGATGTGGAGATCTCATATGTCA	441		
OY	351	ATGCCCCCAGTCAATGGGTCACAGCAATCCAAAGTGGTGGTATGAGTACAAATATT	410		
Db	442	AGTGAACCTACTCTCTGCTGCTTCTGCAATCCAAGCTGTATGACAGATCTCAGATT	501		
OY	411	GACTTGGTGTAGGGCCAAAGACTCCCAACGAGTGGTGGACATTATACAGGTTGT	470		
Db	502	GCTATGTGGTGTAGGACCAAAAGAGTCCCAATGCAGTTGTGGACATTATCTCAGCTGT	561		
OY	471	TGGTACTGCTTACCTGCTGGTGGATGGGAATGGCTACTGCCCCAATCAAAAGTTCTA	530		
Db	562	TGGTACTGACTTACAGAGTAGGCTGTGGAAATGGCTACTGCCCCAATCAAAAGTTCTA	621		
OY	531	AAATACTACTATGTTGGCCAAATATTTGCTGCTGTTAATGGCTAATAGACTATATGTC	590		
Db	622	AAATACTACTATGTTGGCCAAATATTTGCTGCTGTTAATATGATATGAAGAATATCC	681		
OY	591	CCTTATGAACAAGAGCACCTTGTGCCAGTGTCCCAAGTACTGTGACAGATGCACTATGC	650		
Db	682	CCGTGACCAACAAGAGCACCTTGTGCCAGTGTCCCAAGTACTGTGACAGATGCACTATGC	741		
OY	651	ACCAATGGTTCAGATAGCAAGATCTCTATAGTAACTGTAAAGTTTGAAGTCACATTA	710		
Db	742	ACCAATAGTTCGACAGTATCAAGATCTCTCTAGTAACTGTGATTCCTTGAAAGT--ACAGCT	800		
OY	711	ACCTGTAAACACTAGTGTGTCAGGACAGTTCGCAAGGCATCTGCAATGTGTTCAAAACAGC	770		
Db	801	GCGTGTGAACATGATTTACTCMAGCAAAAGTNCAGGCTACTTGGCTATGTGAGACAAAA	860		
OY	771	ATTATTAATAATAGCATTAACACACCGAGTAGGGCATATGAGAGAGAGTCAATATATCTA	830		
Db	861	TTNACTGATTNACCTAGTAGAGCATTTGTCCAMAGACTGCATGATTAAGNCTGCATCATTTTA	920		
OY	831	CTT 833			
Db	921	ATT 923			
RESULT 9					
LOCUS	BMS54122	103 bp	mRNA	linear	EST 20-FEB-2002
DEFINITION	AGNCCOURT.6546919 NIH_MGC_119 Homo sapiens CDNA IMAGE:5742354				
ACCESSION	BMS54122				
VERSION	BMS54122.1	GI:18793449			
KEYWORDS	EST.				





/tissue\_type="metastatic prostate bone lesion"  
 /lab\_host="DH10B"  
 /note="Vector: PAMPI0; mRNA made from metastatic prostate lesion of the bone, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Library made by D. Kitzman, NIH."  
 BASE COUNT 178 a 82 c 89 g 134 t  
 ORIGIN

Query Match 21.3%; Score 455.6; DB 9; Length 483;  
 Best Local Similarity 97.1%; Pred. No. 2.6e-61;  
 Matches 464; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 1607 ACAAAATGACGCTTCCACAGTATCAAAATTAACGTCACAGTATGATTCAGAT 1666  
 DB 6 ACTACTAAATTCGCGCGCGTCGACAAAATTAAGCTCACGATGATTCATTCAGAT 65  
 OY 1667 TTGTTCTGATATATTTCTTAATAATTCATATCCCAATCTAATATGAGCTAAACATC 1726  
 DB 66 TTGTTCTGATATATTTCTTAATAATTCATATCCCAATCTAATATGAGCTAAACATC 125  
 OY 1727 CAGCAAACTCAAGTGAAGGACATTCACAAAATATCCCTGGGTATTTTAGAGTATTC 1786  
 DB 126 CAGCAAACTCAAGTGAAGGACATTCACAAAATATCCCTGGGTATTTTAGAGTATTC 185  
 OY 1787 TCAAAACGTGTAATAATCATGCAAAATTAAGCAATCCTGAGAAACATCAGACACATG 1846  
 DB 186 TCAAAACGTGTAATAATCATGCAAAATTAAGGGAATCCTGAGAAACATCAGACACATG 245  
 OY 1847 AGACTAAGAGACATGTGAGCCAAATGCATGTGCTTGTGATCAGATCCCGAAGACGA 1906  
 DB 246 AGACTAAGAGACATGTGAGCCAAATGCATGTGCTTGTGATCAGATCCCGAAGACGA 305  
 OY 1907 AAAAGATCAGTAATGAAAAAATGTAAGTCTGAATAGAAATCTGAGATATTTTAAACG 1966  
 DB 306 AAAAGATCAGTAATGAAAAAATGTAAGTCTGAATAGAAATCTGAGATATTTTAAACG 365  
 OY 1967 TAGCTGATTTCTTAATCTTGACAAATATATGACAGGATATGATAGATAGATACCTTGA 2026  
 DB 366 TAGCTGATTTCTTAATCTTGACAAATATATGACAGGATATGATAGATAGATACCTTGA 425  
 OY 2027 GAAATGAAACTGGGTGAGGGCTATCTAGAAATCTCTGTAATCTTACCAATTTT 2084  
 DB 426 GAAATGAAACTGGGTGAGGGCTATCTAGAAATCTCTGTAATCTTACCAATTTT 483

RESULT 11  
 BF897377/c 462 bp mRNA linear EST 18-JAN-2001  
 LOCUS BF897377 1123-281100-265-405 MT0181 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF897377  
 VERSION BF897377.1 GI:12288836  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 462)  
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 MEDLINE 20202663  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=IL2et2-IL2-MT0181-281100-265-A05et3-2000-11-28et4-1)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 461.  
 Location/Qualifiers  
 1. 462  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_11b="MT0181"  
 /dev\_stage="Adult"  
 /note="Organ: marrow; Vector: puc18; Site.1: Sma1; Site.2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 131 a 99 c 94 g 136 t 2 others  
 ORIGIN

Query Match 21.2%; Score 453.6; DB 12; Length 462;  
 Best Local Similarity 98.7%; Pred. No. 5.4e-61;  
 Matches 456; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 307 ATCGAATGACAGTGAATAATGCTGAGAAATCTATACATGCAAGTCCCCACTAT 366  
 DB 462 ATCGAATGACAGTGAATAATGCTGAGAAATCTATACATGCAAGTCCCCACTAT 403  
 OY 367 GGTCAAGCAATCCAAAGCTGTTGATGAGTACATGATTTTACTTTGGTGAAGGC 426  
 DB 402 GGTCAAGCAATCCAAAGCTGTTGATGAGTACATGATTTTACTTTGGTGAAGGC 343  
 OY 427 CAAAGCTCCCAAGCCAGTGTGACATATACACAGGTTGTTGTAATCTTCAATAC 486  
 DB 342 CAAAGCTCCCAAGCCAGTGTGACATATACACAGGTTGTTGTAATCTTCAATAC 283  
 OY 487 TCGTGGATGGGAATGCTCTACTCTCCCAATCAAAAGTTTAAATATCTATGTT 546  
 DB 282 TCGTGGATGGGAATGCTCTACTCTCCCAATCAAAAGTTTAAATATCTATGTT 223  
 OY 547 GCCAATATTTGCTGCTGCTGTAATGGCTAATAGACTATATGCTTATGCAAGAG 606  
 DB 222 GCCAATATTTGCTGCTGCTGTAATGGCTAATAGACTATATGCTTATGCAAGAG 163  
 OY 607 CACCTTGCCAGTGTGCCAGATACTGTGAGATGAGATGACCAATGGTTCAAGT 666  
 DB 162 CACCTTGCCAGTGTGCCAGATACTGTGAGATGAGATGACCAATGGTTCAAGT 103  
 OY 667 ACGAAGATCTGATAGTAACTGTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTT 726  
 DB 102 ACGAAGATCTGATAGTAACTGTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTT 43  
 OY 727 TGGTCAGGAGCAGTGAAGGATCTGCAATGTTTCAACA 768  
 DB 42 TGGTCAGGAGCAGTGAAGGATCTGCAATGTTTCAACA 1

RESULT 12  
 A1791346 455 bp mRNA linear EST 13-DEC-1999  
 LOCUS A1791346  
 DEFINITION nh30h09.y5 NCI\_CGAP\_P13 Homo sapiens cDNA clone IMAGE:953921, mRNA sequence.  
 ACCESSION A1791346  
 VERSION A1791346.1 GI:5339062  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens





BASE COUNT	138 a	94 c	96 g	122 t	ORIGIN
Query Match	20.9%	Score 448.4	DB 12	Length 450	
Best Local Similarity	99.8%	Pred. No. 3,5e-60			
Matches 449	Conservative	0	Mismatches 1	Indels 0	Gaps 0
260	CCAAAAGTGGGCAACCACTGCAATTTACAGACACAGTAAACCAAGAGATGGAATGCANG	319			
1	CCAAAAGTGGGCAACCACTGCAATTTACAGACACAGTAAACCAAGAGATGGAATGCANG	60			
320	TCTAAATGTGTGAGACATCTACATGTCAAGTGGCCCGACGCTATGGTCAAGCAAT	379			
61	TCTAAATGTGTGAGACATCTACATGTCAAGTGGCCCGACGCTATGGTCAAGCAAT	120			
380	CCAAAGCTGTTGATGAGTACATGATTTTGATTTGGTGTAGAGGCCAAAGACTCCNA	439			
121	CCAAAGCTGTTGATGAGTACATGATTTTGATTTGGTGTAGAGGCCAAAGACTCCNA	180			
440	CCGAGGGTGGGCAATTTACACAGGTTGGTGTGACTCTTATACCTGTTGGATGTGG	499			
181	CTCAGTGGTGGGCAATTTACACAGGTTGGTGTGACTCTTATACCTGTTGGATGTGG	240			
500	AAATGCTACTGTCCCAATCAAAAAGTTTAAATACACTATGTTTGGCAATATTGTCC	559			
241	AAATGCTACTGTCCCAATCAAAAAGTTTAAATACACTATGTTTGGCAATATTGTCC	300			
560	TGCTGTGTAATTTGGGCTAATAGACTATATGTCCTTATGGAACAAGAGACACTTGTCCAG	619			
301	TGCTGTGTAATTTGGGCTAATAGACTATATGTCCTTATGGAACAAGAGACACTTGTCCAG	360			
620	TGCGCCAGTACTGTGACGATGAGACTATGACCAATGTTTCCAGTACGAGATCTCTA	679			
361	TTGCCAGATTAATCTGTACGATGAGACTATGACCAATGTTTCCAGTACGAGATCTCTA	420			
680	TAGTACTGTAAAGTTTGAAGCTCACATT	709			
421	TAGTACTGTAAAGTTTGAAGCTCACATT	450			
RESULT 15					
LOCUS	BM559790				
DEFINITION	AGENCOURT.6565524 NIH_MGC_119 Homo sapiens cdna clone IMAGE:5744414				
ACCESSION	BM559790				
VERSION	BM559790.1				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.				
TITLE	1 (bases 1 to 1063)				
JOURNAL	NIH-MGC http://mhc.nci.nih.gov/				
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)				
	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				
	Email: c9apds-remail.nih.gov				
	Tissue Procurement: Life technologies, Inc.				
	CDNA Library Preparation: Life technologies, Inc.				
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)				
	DNA Sequencing by: Agencourt Bioscience Corporation				
	Clone distribution: MGC clone distribution information can be				
	found through the I.M.A.G.E. Consortium/LNL at:				
	http://image.lnl.gov				
	plate: LLM12765 row: 1 column: 15				
	High quality sequence stop: 618.				
FEATURES	Location/Qualifiers				
source	1. 1063				
	/organism="Homo sapiens"				
	/db xref="taxon:9606"				

